**Amendments to the Specification:**

Please replace paragraph [0130] with the following paragraph:

[0130] The ITS sequences (isolate RP38.3, (SEQ ID NO:1); isolate RPK (SEQ ID NO:2)) are then subjected to a similarity search, using the BLAST 2.0 server at NCBI (~~http://www.ncbi.nlm.nih.gov:80/BLAST;~~ Altschul et al., *J Mol Biol* 215: 403-410, 1990). The sequences of the 18S rRNA genes (isolate RP 38.3, (SEQ ID NO:3); isolate RPK (SEQ ID NO:4)) are aligned against other eukaryotic 18S rRNA genes, using the facilities of the Ribosomal Database Project at Michigan State University (~~http://rdp.cme.msu.edu/html/;~~ Maidak et al., *Nucleic Acids Res* **28**: 173-174, 2000). The deduced phylogenetic placement of isolated fungi with $\beta$-glucuronidase activity is shown in Table 3.

Please replace paragraph [0140] with the following paragraph:

[0140] The ORFs are translated into amino acid sequences (see Figure 2, SEQ ID NO:2 and Figure 3 SEQ ID NO:4). Analysis using a neural-network program (SignalP V1.1) trained to recognize eukaryotic N-terminal signal peptides, reveals that both fungal GUS proteins contain signal peptides (~~SignalP V1.1 at http://www.cbs.dtu.dk/services/SignalP~~; Nielsen et al., *Protein Engineering* **12**: 3-9, 1999). The predicted cleavage positions are between amino acids No. 26 and 27 (*Scopulariopsis* sp.) or 18 and 19 (*Penicillium canescens*). The presence of these N-terminal signal peptides suggests that both fungal isolates may produce secreted $\beta$-glucuronidases. This is consistent with the observation that both stain the surrounding agar blue.

Please replace paragraph [0141] with the following paragraph:

[0141] The protein sequences are subjected to a similarity search, using the BLASTP program at the BLAST 2.0 server of NCBI (~~http://www.ncbi.nlm.nih.gov:80/BLAST;~~ Altschul et al., *J Mol Biol* 215: 403-410, 1990). Results of these analyses demonstrate that the gene products are closely related to fungal and mammalian $\beta$-glucuronidases (e values range from $10^{-180}$ to $10^{-53}$). A conserved domain (CD) search at the same server identifies three CDs: pfam02837 (glycosyl hydrolases family 2; sugar-binding domain), pfam02836

(glycosyl hydrolases family 2; TIM barrel domain), and pfam00703 (glycosyl hydrolases family 2; immunoglobulin-like $\beta$-sandwich domain). In addition, both fungal GUS proteins contain the two signatures that, according to the Swiss Institute of Bioinformatics, characterize family 2 glycosyl hydrolases (see ~~http://www.expasy.ch/cgi-bin/nicedoc.pl?~~PDOC00531). This confirms that fungal GUS proteins, like GUS proteins from other organisms, are members of family 2 of glycosyl hydrolases.

Please replace paragraph [0142] with the following paragraph:

[0142] To compare the amino acid sequences of the fungal GUS proteins with those of other $\beta$-glucuronidases, the sequences of other GUS proteins are retrieved from GenBank ~~(http://www.ncbi.nlm.nih.gov/Genbank/)~~. In addition, using the TBLASTN program at the BLAST 2.0 server at NCBI ~~(http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi?)~~, fungal genomes are mined for non-annotated gus genes and translated into proteins.

Please replace paragraph [0144] with the following paragraph:

[0144] The predicted amino acid sequences of these two additional gus genes are used as query sequences in a similarity search using the BLASTP program at the BLAST 2.0 server of NCBI (~~http://www.ncbi.nlm.nih.gov:80/BLAST;~~ Altschul et al., *J Mol Biol* 215: 403-410, 1990). Results of these analyses demonstrate that their gene products are closely related to fungal and mammalian $\beta$-glucuronidases (e values range from $10^{-174}$ to $10^{-79}$). This search also identifies three CDs: pfam02837 (glycosyl hydrolases family 2; sugar-binding domain), pfam02836 (glycosyl hydrolases family 2; TIM barrel domain), and pfam00703 (glycosyl hydrolases family 2; immunoglobulin-like $\beta$-sandwich domain). Furthermore, both fungal GUS proteins contain the two signatures that, according to the Swiss Institute of Bioinformatics, characterize family 2 glycosyl hydrolases (see ~~http://www.expasy.ch/cgi-bin/nicedoc.pl?~~PDOC00531).

Please replace paragraph [0146] with the following paragraph:

[0146] In pair-wise alignments, the overall identity (similarity) to $GUS^{Ecoli}$ is 49.6 % (60.5 %) for *Scopulariopsis* sp. and 50.3 % (61.6 %) for *Penicillium canescens*. The identities at the DNA level are 55.3 % (*Scopulariopsis* sp.) and 50.8 % (*Penicillium canescens*). The overall identity (similarity) to $GUS^{Ecoli}$ is 47.3 % (59.1 %) for *Aspergillus nidulans* and 50.4 % (63.3 %) for *Gibberella zeae*. Like the *Penicillium* and *Scopulariopsis* GUS proteins, the gene product from *Aspergillus nidulans* has an N-terminal signal peptide with a predicted cleavage position between amino acid No. 20 and 21 (~~SignalP V1.1 at http://www.cbs.dtu.dk/services/SignalP;~~ Nielsen et al., *Protein Engineering* **12**: 3-9, 1999). By contrast, the predicted gene product of *Gibberella zeae* does not appear to have an N-terminal signal peptide (Figure 7).